Coordinated increase of nuclear tension and lamin-A with matrix stiffness outcompetes lamin-B receptor that favors soft tissue phenotypes

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ABSTRACT Matrix stiffness that is sensed by a cell or measured by a purely physical probe reflects the intrinsic elasticity of the matrix and also how thick or thin the matrix is. Here, mesenchymal stem cells (MSCs) and their nuclei spread in response to thickness-corrected matrix microelasticity, with increases in nuclear tension and nuclear stiffness resulting from increases in myosin-II and lamin-A,C. Linearity between the widely varying projected area of a cell and its nucleus across many matrices, timescales, and myosin-II activity levels indicates a constant ratio of nucleus-to-cell volume, despite MSCs' lineage plasticity. Nuclear envelope fluctuations are suppressed on the stiffest matrices, and fluctuation spectra reveal a high nuclear tension that matches trends from traction force microscopy and from increased lamin-A,C. Transcriptomes of many diverse tissues and MSCs further show that lamin-A,C's increase with tissue or matrix stiffness anti-correlates with lamin-B receptor (LBR), which contributes to lipid/sterol biosynthesis. Adipogenesis (a soft lineage) indeed increases LBR:lamin-A,C protein stoichiometry in MSCs versus osteogenesis (stiff). The two factors compete for lamin-B in response to matrix elasticity, knockdown, myosin-II inhibition, and even constricted migration that disrupts and segregates lamins in situ. Matrix stiffness-driven contractility thus tenses the nucleus to favor lamin-A,C accumulation and suppress soft tissue phenotypes.

INTRODUCTION As a cell adheres and pulls on its surroundings (Nicolas et al., 2004; Discher et al., 2005; Sawada et al., 2006; Levental et al., 2009; Gardel et al., 2010; Kassianidou et al., 2017), the shape of the nucleus changes in a manner similar to the shape of the cell—as quantified long ago (Weiss and Garber, 1952). The stiffness of a cultured cell's microenvironment is now understood to drive the spreading and flattening of most types of cells (Pelham and Wang, 1997) and their nuclei (Swift et al., 2013). Such studies have typically used gel matrices that are thick relative to the size of a cell. However, thin matrices present a means to maintain constant gel chemistry and surface density of adhesion ligand as a function of matrix thickness, h (Engler et al., 2006; Hadden et al., 2017), with early studies showing that soft gels on top of rigid substrates can drive spreading when minimal polymer is used (Ben-Ze’ev et al., 1980). Thin layers of extracellular matrix are also evident in some tissues, including the collagenous “osteoid” film on top of calcified bone, which promotes osteogenesis (Sodek and McKee, 2000). Although studies of the interplay between nucleus and cytoskeleton in cells cultured on matrices of controlled elasticity and/or thickness remain limited (Buxboim et al., 2014; Alam et al., 2015), plating of cells on surfaces with different mechanical properties has been well studied in terms of the effects on the acto-myosin cytoskeleton (Beningo et al., 2004; Engler et al., 2004b; Prager-Khoutorsky et al., 2011;
Talele et al., 2015; Meacci et al., 2016; Kassianidou et al., 2017). Tensions generated by the cytoskeleton propagate into any flexible matrix, and the resistance sensed by a cell can include an underlying hidden rigidity—like the proverbial “princess and the pea.” However, many quantitative aspects of mechanical depth-sensing remain obscure, particularly nuclear phenotypes that include the nuclear-to-cell volume ratio (Kume et al., 2017). Such features can be complicated for stem cells including the mesenchymal stem cells (MSCs) studied here because phenotype-defining changes in gene expression occur in differentiation.

The nuclear envelope is composed of the nuclear lamina proteins plus many more factors that attach the lamina to the nuclear membrane or link it to the cytoskeleton (Goldman et al., 2002; Gruenbaum et al., 2005). Akin to keratins of nails or hair, lamins are nuclear intermediate filament proteins that assemble into ~300–600 nm multimers (Turgay et al., 2017) in juxtaposed meshworks of A-type versus B-type lamins (Shimi et al., 2008). Across tissues, lamin-A,C varies widely but increases systematically with tissue stiffness, and the in vitro levels of lamin-A,C have also been found to be matrix-mechanosensitive in MSCs and other cell types (Swift et al., 2013). The roundworm Caenorhabditis elegans likewise shows less lamin in neuronal tissue (soft) compared to muscle tissue (stiff) (Zuel et al., 2016). Interphase phosphorylation of lamin-A,C (Kochin et al., 2014) favors its turnover in cells on soft matrix (Buxboim et al., 2014). In comparison, B-type lamins differ minimally across solid tissues and do not exhibit much interphase phosphorylation. Lamin knockout mice generate all embryonic lineages (Kim et al., 2013), but lamin-A and -C nulls die within weeks of birth with defects only in stiff tissues, including contractile heart and skeletal muscle (Sullivan et al., 1999; Kubben et al., 2011). Key relationships between lamins, other nuclear envelope proteins, and the acto-myosin cytoskeleton are thus emerging, but there is still a need to understand the effective stiffness and/or thickness of matrix in relation to cytoskeletal tension, nuclear stress, and tissue-relevant differentiation. Here we estimate the nuclear-to-cell volume ratio and changes in nuclear envelope tension as MSCs spread on gels of varied stiffness and thickness, and then we place the in vitro findings in a tissue context that takes advantage of MSC lineage plasticity. Our findings help identify lamin-B receptor (LBR), which contributes to lipid/sterol synthesis (Subramanian et al., 2012), as an additional matrix-mechanosensor in the nucleus that is downstream from nuclear tension and lamin-A,C.

RESULTS

Cells sense rigidity that is buried in soft matrices

Sparse cultures of MSCs on soft-and-thin gels (1 kPa, 3–15 µm; Buxboim et al., 2010b) that are collagen-functionalized show greater cell spreading and more prominent stress fibers of myosin-II than cells cultured on soft-and-thick matrices (>35 µm) made in parallel (Figure 1Ai). Stiff matrices (e.g., 40 kPa) promote both spreading (Pelham and Wang, 1997; Engler et al., 2004a) and stress fibers (Yeung et al., 2005); MSCs clearly feel through thin gels to the rigid glass beneath. Even with matrices of intermediate stiffness (10 kPa), differences are evident between thin and thick matrices of the same stiffness E (Figure 1Aii). Nuclei exhibit the same trends in spreading as cells, consistent with past observations of morphologies on diverse matrices (Weiss and Garber, 1952). Simple hyperbolic models (Zemel et al., 2010) typically fit cell spreading as well as nuclear spreading (Supplemental Figure S1) in the coupled processes of protrusion, matrix binding, and myosin-II-driven contraction resisted (or not) by matrix. Such spreading profiles reveal tactile length scales (hn) for both cells and nuclei that systematically decrease from ~25 µm for soft matrices to ~0 µm for very stiff matrices.

Collecting all morphology results for all matrices together shows that a linear relationship between projected areas of cells and nuclei (Figure 1Aiii) is maintained, even when sensitivity to matrix elasticity is inhibited by relaxing cells with the myosin-II inhibitor, blebbistatin (blebb). An invariant ratio of cell-to-nuclear projected areas is a key biophysical parameter that is independent of microenvironment even for high passage MSCs that spread more, express distinct markers of differentiation such as α-smooth muscle actin (Dingal et al., 2015; Talele et al., 2015), and eventually become senescent (Supplemental Figure S1). As a function of adhesion time on rigid substrates, cell and nuclear spreading achieve within ~1 h the same proportionality as the steady-state morphologies on gels of different stiffness (Figure 1B and Supplemental Figure S2). Rigid substrates allow for nanoresolution imaging by atomic force microscopy (AFM) of dried samples that show the expected round cell morphology that breaks symmetry with spreading (Yam et al., 2007; Prager-Khoutorsky et al., 2011; Wolfenson et al., 2014). Consistent with such past studies, the accompanying fluorescence images for actin and myosin-IIA confirm the leading edge polymerization of the dense actin meshwork with myosin-II further back that assembles into both radial and circumferential stress fibers (Figure 1C). A muscle-inspired, Hill-type model of cell spreading is thus suggested: the steady state in retrograde actin flow is tuned by myosin-II minifilaments pulling F-actin back quickly (on soft matrix) or slowly (on stiff matrix), such that the load or resistance is provided by matrix elasticity (Figure 1D).

A systematic flattening of the spread nucleus on stiffer matrices is evident in confocal z-stacks of hydrated samples (Figure 1Ai, bottom). For all substrates the bottom of the nucleus is nearly in contact with the underlying substrate (Figure 1Aiii, inset images), and the top of the nucleus is near the maximum height of the cell. These observations suggest that the height of the nucleus can limit the spreading of the cell. This idea is mathematically formulated in a nuclear height model of spreading that yields an invariant ratio of cell-to-nuclear volume (see Materials and Methods: Nucl-Ht Model). Cell-to-nuclear volume ratio is a long-recognized characteristic of a given cell type (Kume et al., 2017) and is, for example, small with embryonic stem cells. However, the MSC results here further indicate that this key biophysical characteristic is independent of both time and matrix elasticity as well as senescence and the associated differentiation, although other lineages need to be studied further. Factors that control nuclear height or volume, including both transport factors (Kume et al., 2017) and osmolarity (Irianto et al., 2013), will thus regulate spreading of both the cell and its nucleus. Based on the matrix-desensitizing effects of blebbistatin (Figure 1), such factors certainly also include the stress applied by the cytoskeleton on the nucleus.

Cells sense an apparent microelasticity that accounts for geometry

A soft-and-thin gel is clearly equivalent to a stiff-and-thick gel of high stiffness in terms of cell and nuclear morphology. Physical probing of a soft-and-thin gel with the tip of an atomic force microscope indeed yields a high value for the “apparent” microelasticity (µ-elasticity; Figure 2A). Remarkably, all of the data for cell and nuclear projected areas versus the apparent µ-elasticity measured by AFM fitted a “universal” Hill-type curve with half-max (µE) between soft and stiff of ~4 kPa (Figure 2B).

Compared to soft-and-thick matrices, MSCs on soft-and-thin or stiff matrices produce high contractile forces, with a progressive increase in apical stress fibers above the nucleus, that stretch and squash the otherwise wrinkled nucleus against the matrix. Nuclear height measurements of ~3 µm by AFM (Figure 3A) are consistent with confocal imaging (Figure 1A). Fourier spectra of quenched
nuclear fluctuations or roughness, top-and-bottom averaged per cell and smoothed across many nuclei shows that the mean amplitude of the wrinkles (U) decays with wave number q (Figure 3B). The scaling (~1/q) is reminiscent of the tension-suppressed undulations on lipid membranes (Sackmann, 1994). According to such a model, the approximate twofold suppression of wrinkle amplitude from soft matrix to rigid substrate corresponds to an approximate fourfold increase in nuclear tension or stress, σ. Traction force microscopy applied to MSCs shows that the cell tensions in the midplane of the cell near the nucleus likewise increase approximately fourfold from similarly soft to stiff substrates (Figure 3C; Engler et al., 2006). Nuclei of cells on soft-and-thin substrates are thus under intermediate tension. Sustaining such nuclear tension is the expected role for the main structural proteins of the nucleus, the lamins, but evidence of this was sought from expression profiles of cells on various soft matrices and in diverse tissues.

Mechanosensitive nuclear envelope: four genes in vitro and in vivo

Gene expression profiles of MSCs differ significantly after just 24 h on matrices of varied elasticity and thickness as well as standard plastic flasks, particularly for some of the most widely studied nuclear envelope structural components (Figure 4A). Key components include the three lamin isoforms (LMNA, LMNB1, LMNB2), four nesprins (SYNE1 to SYNE4), and 11 more components involved in linking the lamina to the nesprins or the nuclear envelope to chromatin, such as the lamin-B receptor, LBR. Dendrogram clustering of the heat map comparing all conditions to soft-and-thick matrix shows the expression profiles for stiff gels and soft-and-thin gels are similar to plastic (Pearson correlation 0.9), consistent with these latter substrates feeling rigid to cells. Importantly, LMNA anti-correlates with LBR (Pearson: p = −0.3) in this matrix mechanosensing by the nucleus.

Anti-correlations of LMNA and LBR have been reported in other contexts (Solovei et al., 2013), and so to begin assessing whether such relationships are generic, we partially knocked down, 2013), and so to begin assessing whether and in vivo contexts (Solovei et al., 2013); the nesprins link the nucleus and cytoskeleton to transmit stress to the nuclear envelope (Starr and Fridolfsson, 2010) and understandably vary greatly between tissues under different stresses. However, the LBR variations motivated study in broader contexts.

Hematopoietic stem cells and progenitors (HSCPs) are bone marrow derived as are MSCs, but HSCPs do not adhere and spread on plastic, which is how MSCs are classically isolated (Supplemental Figure S3). Marrow is of course very soft, and the human HSCPs indeed show low LMNA levels compared to MSCs (Figure 4A, third heatmap) consistent with low levels of lamin-A,C protein in HSCPs and a soft nucleus (Pajerowski et al., 2007). Nuclear envelope genes that show the largest %-difference in HSCPs relative to MSCs are again LMNA, SYNE1, SYNE2, and LBR, with a clear anti-correlation between LBR and LMNA. In neutrophils that derive from HSCPs, lamin-A,C is strongly down-regulated and LBR increases, with LBR's sterol reductase domain being important to lipid droplet formation (Subramanian et al., 2012). Given that HSCPs are not strongly adherent cells, they might not need much myosin-II to mechanosensate matrix (Engler et al., 2004a; Raab et al., 2012). Transcript levels of MYH9 are indeed low in HSCPs, and MYH9 generally correlates with LMNA across conditions. In contrast, the constitutively expressed heat shock stress gene HSP90 isoform, HSP90AB1, remains nearly constant across all conditions.

Human and mouse tissue profiles show that LMNA, LBR, and SYNE1,2 are the most mechanosensitive nuclear envelope genes in five tissues that range from soft (brain) to stiff (heart) (Figure 4C, right plot). In these plots of the coefficient of variation across the same five tissues (soft to stiff: brain < liver < kidney < skeletal muscle ~ heart), we take as the most reliable measure for a given gene the species with the smallest variation (man or mouse). Although all tissues are now understood to harbor MSCs as perivascular cells with a highly plastic phenotype (Crisan et al., 2008), it is surprising that a single stem cell type in culture, the MSC, shows the same four components with the same trend in variation, that is, SYNE2 > SYNE1 > LMNA > LBR. For the broad range of human and mouse tissues, systematic relationships were then sought between LMNA and LBR as well as myosin-II isoforms (MYH9) that vary widely across tissues. Transcript ratios for (LBR per LMNA) and (most abundant MYH9 per LMNA) plotted versus LMNA provide a measure of stoichiometry changes relevant to directly competitive as well as indirectly synergistic association networks, and LMNA is of course expected to increase with tissue stiffness (Figure 4D). The softest tissue profiled is brain (from ectoderm), which shows the lowest relative levels of LMNA and MYH9 but also the highest relative level of LBR. For the other nonmuscle tissues (mostly endodermal) we find MYH9 has
**FIGURE 1:** Cells feel many microns into soft microenvironments. (A) (i) Mesenchymal stem cells (MSCs) and their nuclei are spread more on gels that are soft-and-thin (1 kPa; 2–3 μm) compared to soft-and-thick (~35 μm) at 24–36 h in culture (scale bars = 10 μm). Bottom, x-z contours of lamina from confocal stacks of immunostained lamin-A,C. Nuclear height (average ± SEM; n > 25) is maximal on thick and soft gels but nuclei become increasingly flattened on thin-and-soft gels (p = 0.006) and rigid glass (p < 0.001). (ii) Mean projected areas of nuclei and cells vs. matrix thickness. Hill function exponents are α = 0.8 and 15 for 1 and 10 kPa gels, respectively. Tactile length scales are defined as the thickness below which cells or nuclei spread more than a measurable 10% relative to cells on thick gels of the same E; h_t = 25 μm for 1 kPa, h_t = 15 μm for 10 kPa, and h_t = 0 μm for 40 kPa, making the latter indistinguishable from collagen-coated glass.
FIGURE 2: The apparent microelasticity sensed by a cell on thin or thick gels is similar in trend to that measured by an inanimate probe. (A)(i) AFM force-indentation representative curves show a sharp deflection of the cantilever on gels that are soft (1 kPa) but thin. Gel contact points are at the origin. (ii) Apparent microelasticity ($\mu$-elasticity) of polyacrylamide gels, as measured by AFM nanoindentation, is plotted as a function of the elastic modulus (bulk stiffness calibrated by desktop rheometer) and thickness. While AFM nanoindentation of thick gels shows agreement with gels’ elastic moduli, $\mu$-elasticity increases with decreasing gel height, exhibiting effective stiffening at the micron scale most profoundly for soft gels. (B) As the spreading of cells (i) and the projected area of nuclei (ii) are distinctively shown to increase with gels’ stiffness and thickness (Figure 1Aii and Supplemental Figure S1B), we plot them here as a function of the apparent matrix $\mu$-elasticity. Cell and nucleus data (average ± SEM, n > 25 cells) are collectively fit to $f(x) = A \cdot \frac{x^n}{x^2 + E_{\mu}^2} + b$, with an exponent of cooperativity $n = 0.5$. The transition between soft and stiff matrices is set by $E_{\mu}$ amounting to 4–4.5 kPa, thus discriminating between compliant tissues such as brain, marrow, and fat and stiffer tissues such as muscle, cartilage, and bone.

again the highest gene expression among myosin-II isoforms, which is consistent with myosin-IIA being most abundant in MSCs at the transcript level here and at the protein level in both MSCs (Raab et al., 2012) and related cell lines (Ma et al., 2010). For muscle tissues (mesoderm), the most abundant isoforms are MYH1,2 in skeletal muscle and MYH6,7 in heart, and the expression levels of these isofoms in highly contractile tissue lie understandably above the MYH9 curve, consistent with tissue-specific regulation of distinct genes. Nonetheless, these muscle tissues are the stiffest tissues profiled here, and have the highest LMNA levels and the lowest LBR. All of these trends in transcriptomes suggest mechanosensing involves an anti-correlated expression of lamin-A,C and LBR, which should be scrutinized at protein levels, starting with a tissue-relevant context of differentiation.

Adipogenesis (soft) favors LBR, while osteogenesis (stiff) favors lamin-A,C

Tissue-relevant functions of MSCs were confirmed in conventional cultures by inducing adipogenesis and osteogenesis as typical soft and stiff tissue lineages, respectively (Figure 5Ai,ii), and then we focused on the cytoskeleton and nucleus. In adipogenesis, lipid droplets completely replace the actin cytoskeleton, and LBR is highly abundant in localizing to the periphery of lipid droplets (Figure 5B). This seems appropriate given LBR’s role in lipid synthesis (Subramanian et al., 2012). Lamin-A,C is lowest in adipogenesis, whereas LBR is highest (Figure 5C, top), consistent with transcriptomics showing of soft lineages and repression of acto-myosin (Figure 4).

Nuclear area is greatest in osteogenesis (Figure 5C, bottom), consistent with matrix stiffness effects (Figure 1A). Indeed, soft- and-thin gels increase osteogenesis of MSCs relative to soft-and-thick gels with the same $E$ (1 kPa; Figure 5D). This finding is in line with osteoid being a thin layer of matrix on rigid bone (Sodek and McKee, 2000; Buxboim et al., 2010a). Such differentiation takes many days, whereas cell and nuclear morphology changes occur within hours (Figure 1B and Supplemental Figure S2). This considerable difference in time scales raised questions about the interactions of lamin-A,C, LBR, and myosin-IIA in the absence of differentiation.

(i.e., “rigid”). Blebbistatin (Blebb) inhibits myosin-II and eliminates spreading differences on different matrices.

(iii) Linearity of cell vs. nucleus projected area is maintained across matrices of different elasticities and thicknesses and is also satisfied by Blebb-treated myosin-inhibited cells. Inset images of x-z cross sections show spread cell height is constrained by nuclear height. (B) Cell vs. nuclear spreading kinetics on rigid glass (red) tracks the “steady-state” projected area of cells on diverse gels (blue) or with myosin-II inhibition by Blebb (green). (C) The dynamics of cell adhesion and spreading were interrogated by AFM (top) and immunostaining (bottom) to show organization of protein of interests with z-axis topography. MSCs were cultured in a standard cell-culture plastic plate and fixed at times ranging between 1 h and 1 d. To facilitate AFM imaging, cells were lipid-membrane stripped and air dried before immunostaining. With adhesion time, cells increasingly spread, and nuclei stretch and flatten down against the substrate and prominent stress fibers developed, consistent with increased generation of contractile forces. At 1 h, cells maintain a spherical morphology and stress fibers are radially distributed (yellow arrowheads, zoom-in images) with a wide lamellipodium structure (red arrowheads) but after 4 h of adhesion symmetry is broken and within 24 h cells obtain a typical mesenchymal-like morphology typical of stiff matrices. Unlike the immunofluorescence (IF) images, AFM micrographs are in scale (scale bar: 10 µm). z-Axis heights measured by AFM is an underestimate, due to fixing, membrane-stripping, and dehydration of the cells. (D) A simple Hill-type model of cell spreading in which myosin-II rectifies F-actin polymerization depending on the resistance provided by matrix elasticity.
FIGURE 3: Nuclear roughness is suppressed by matrix stiffness, yielding an estimate of increased nuclear tension. (A) Nanoscopic imaging by atomic force microscopy (AFM) of a membrane-stripped but hydrated MSC shows apical stress fibers that flatten the nucleus against the matrix (red arrow). Nucleus-draped fibers quantified by AFM and by immunofluorescence of myosin-IIA increase in number with adhesion time. (Bi) Lamin-A,C immunostained MSCs imaged by confocal fluorescence microscopy have apical and basal contours of the nuclear envelope that exhibit larger wrinkles on soft gels (0.3 kPa) than on rigid substrates (average ± SEM, n > 25 cells). (ii) The amplitude of nuclear wrinkles is quantified by Fourier-transformed spectra $U(q)$ vs. spatial wave number $q$. Averaged across apical and basal profiles of all nuclei and smoothed, $U(q)$ decreases as $-1/q$ with a prefactor related to nuclear stress $\sigma$ based on wrinkled membrane theory (i.e., $1/\sigma^{\frac{1}{2}}$). (C) Traction force microscopy (Engler et al., 2006) indicates an increase in nuclear stress $\sigma$ in cells on soft gels vs. stiff gels (average ± SEM, n > 10 cells) that is similar to that estimated from wrinkled membrane theory.

Matrix stiffness coordinately increases myosin-IIA and lamin-A,C

Consistent with our recent studies (Swift et al., 2013) and those of others (Hadden et al., 2017), lamin-A,C nuclear intensities are lower in cells on soft matrices (Figure 6Ai), as confirmed by immunoblotting after a few hours of adhesion (Figure 6Aii). The increase of lamin-A,C with matrix stiffness is also greatest with low passage MSCs (Supplemental Figure S1), and a positive correlation in single cell analyses between mechanosensitive lamin-A,C levels and the projected area of nuclei was particularly evident with fresh MSCs that were stressed in isolation by fluid shear (Supplemental Figure S3). Importantly, cells on stiff matrix also express more myosin-IIA (Figure 6Bi), consistent with more stress fibers (Figure 1). Decreased spreading of MSCs on stiff substrates with both blebbistatin or
knockdown of myosin-IIA (siMIIA) is accompanied by decreases in both myosin-IIA and lamin-A,C protein (Figure 6Bii) and transcript (Supplemental Figure S4). LBR shows the opposite response. Likewise, increases in cell and nuclear spreading with adhesion time (Supplemental Figure S2) show increased myosin-IIA and lamin-A,C unless inhibited by blebbistatin (Supplemental Figure S5). Inhibition of myosin-IIA indeed disassembles stress fibers within hours (Engler et al., 2006; Raab et al., 2012). Myosin-IIA and lamin-A,C thus respond in a highly coordinated fashion to matrix mechanics, myosin inhibition, and adhesion time.

The finding that myosin-II contractility regulates nuclear morphology and ultimately impacts lamin-A,C expression is perhaps reasonable, but the reciprocal relationship also seemed likely because lamin-A,C interacts with nuclear actin and other actin-binding proteins (Holaska et al., 2004; Zastrow et al., 2004) that might regulate the transcription factor SRF, which controls MYH9 transcription (Olson and Nordeim 2010). Partial knockdown (KD) of lamin-A,C in MSCs shows, by quantitative immunofluorescence, that myosin-IIA levels are similar in wild-type (WT) and KD cells after just 1 h of adhesion on rigid coverslips starting with suspended cells (Supplemental Figure S5). However, 2 h after adhesion begins, both myosin-IIA and (of course) lamin-A,C remain low in the siLMNA treated cells, whereas myosin-IIA levels have increased in WT cells together with lamin-A,C (consistent with cell and nuclear spreading; Figure 1 and Supplemental Figure S2). At 36 h, a similar difference in both proteins was evident in lysates by both standard immunoblotting and by mass spectrometry quantitation of a dozen or more peptides from each protein (Supplemental Figure S5).

Overexpression of transduced GFP-LMNA (OE) sustained high levels of lamin-A (Supplemental Figure S4), and with increasing lamin-A in A549 lung-epithelial cells the stiffness of the nucleus increased based on micropipette aspiration (Supplemental Figure S4). The effective nuclear elasticity scales with the square root of lamin-A,C and nuclear roughness (Harada et al., 2006; Raab et al., 2012), and that LBR binds lamin-B (as discussed further below), and that abundance of expression in cells on soft, soft-and-thin, and stiff matrices, nuclear LBR decreased as expected with lamin-A,C and collapsed onto a single hyperbolic curve consistent with competitive inhibition (Figure 6Ei). Such a fit suggests that lamin-A,C can outcompete LBR for binding to lamin-B (Ye and Worman, 1994). Knockdown of lamin-A,C indeed increases overall LBR by immunoblotting (Figure 6Eii). Consistent with an indirect coupling to contractility through lamin-A,C, LBR is also up-regulated by knockdown of myosin-IIA (Figure 6Eiii). Knockdown of myosin-IIA as well as LMNA in mesenchymal-like A549 cells (Ye and Worman, 1994) likewise shows the respective decrease or increase in stoichiometry of LBR per LMNA (Supplemental Figure S6). The LBR results thus reinforce the working model of a link between matrix stiffness, contractility, and lamin-A,C.

An alternative approach to visualizing the complementary localization of LBR and lamin-A,C in stressed nuclei was taken with the A549 cells after constricted migration. Nuclear blebs enriched in lamin-A,C and depleted in lamin-B have been seen at one or both ends of the elongated nuclei postmigration (Harada et al., 2014). Immunostaining reveals that LBR is always depleted from the nuclear bleb (Figure 7). One simple interpretation of such images is that LBR binds lamin-B (as discussed further below), and that abundant lamin-A,C somehow obstructs and thereby outcompetes the lamin-B interaction with LBR.

**DISCUSSION**

**Microenvironments influence nuclear phenotypes**

Although a constant cell-to-nuclear volume ratio is a long-recognized characteristic of a given cell type (Kume et al., 2017), it is not obvious that it should apply to a stem cell such as an MSC under diverse adhesion and spreading conditions (Figure 1) that greatly influence differentiation (Engler et al., 2006; Swift et al., 2013). Differentiation of hematopoietic stem cells, for example, yields lineages that have zero nucleus-to-cell volume ratio (red blood cells), small nucleus-to-cell volume ratio (neutrophils), and a larger nucleus-to-cell volume ratio (T-cells). The correlations for MSCs are nonetheless clear in suggesting a constant cell-to-nuclear volume ratio. Matrix elasticity might therefore be an early inductive cue for lineage specification, so that definitively differentiated cells such as those filled with lipid droplets in adipogenesis or else undergoing
FIGURE 4: Transcript profiles reveal mechano-responsive nucleo-structural genes. (A) Nuclear envelope schematic and variations in transcript levels. Consistent with matrix-directed morphologies of nuclei, heatmaps of MSCs cultured (for 36 h) on soft-and-thin gels correlate best with cultures on rigid plastic: Dendrogram shows a Pearson correlation $r = 0.9$. Absolute gene expression intensities averaged across matrix conditions are color-coded by gene symbols (e.g., MYH9 is high, LMNA is intermediate, SYNE2 is very low). Second heatmap: Knockdown of lamin-A produces a low contractility MSC phenotype with down-regulation of MYH9 relative to nontreated (NT) or scrambled siRNA (SC). Third heatmap: Hematopoietic stem cells and progenitors (HSCPs) likewise exhibit a low contractility phenotype with low MYH9 levels correlating with LMNA. In all heatmaps, LBR is anti-correlated. Fourth heatmap: Technical noise across triplicate hybridizations on three microarrays is <$4\%$ on average and no greater than $7\%$ STD of mean intensity. Bottommost “housekeeping” genes validate intensity ($n = 3$ unless indicated). (B) Whole-genome transcriptome changes as indicated after LMNA knockdown. (C) Four mechano-malleable nuclear envelope genes (LMNA, SYNE1, SYNE2, and LBR) exhibit maximal transcriptional variation (STD normalized by mean) across matrix elasticity and thickness conditions in MSC cultures (left) and also in mouse and human tissues (right) of various stiffnesses (brain, liver, kidney, skeletal muscle, etc.).
osteogenesis (Figure 5) should have nucleus-to-cell volume ratios carefully quantified for comparison.

Nuclear flattening and nuclear smoothing with spreading on stiff versus soft matrices are clear (Figures 1 and 4), and the latter suggests about a fourfold increase in tension on the nucleus, which is in agreement with both traction force estimations and changes in lamin-A,C (Figure 6). However, it is unclear whether such tensions (or other mechanisms) can drive decreases in nuclear volume in cells on stiff matrices, given that the nucleus-to-cell volume ratio remains constant. Nuclear volume changes can certainly occur in parallel with cell volume changes when the external osmolarity of a cell medium is altered (Irianto et al., 2013). The latter study approximated both cells and nuclei as ellipsoids and fitted the data to a van der Waals–type model that applies widely to nonideal fluids with excluded volume: water can certainly be extracted from the nucleus, but the nuclear envelope is impermeable to DNA, and so DNA concentration increases when water is extracted (Irianto et al., 2016). The ellipsoidal approximation of nuclear shape was therefore assessed further here in order to describe DNA concentration changes that might result from the decrease in nuclear spreading upon knockdown of lamin-A,C (Figure 6).

Voxel approaches have resolution limits given the large nuclear roughness (Figures 1 and 3), but one simple complementary analysis uses the intensity of Hoechst-labeled DNA (Supplemental Figure S7). Data fits show that nuclear height $H$ multiplied by DNA concentration $[\text{DNA}]$ increases inversely with projected nuclear area $A$ after knockdown, that is, $H[\text{DNA}] \sim 1/A$. Nuclei become taller and $A$ becomes smaller for soft matrix (Figure 1A), and so if $[\text{DNA}]$ remains constant, then $H = 1/A$, which is roughly consistent with observations as well as an ellipsoidal geometry. Furthermore, if DNA concentration does somehow change as a function of nuclear spreading as $[\text{DNA}] \sim A^{-0.5}$, nuclear height must vary as $H \sim A^{0.5}$.
FIGURE 6: Expression profiles of lamin-A,C, myosin-IIA, and LBR are consistent with cell mechanosensitivity. (A) Lamin-A,C levels increase with matrix μ-elasticity (for low passage MSCs, P2), as shown by single cell immunofluorescence at 36 h (i) and also by immunoblot normalized to HSP90AB1 housekeeping levels (ii) after 5 h of cell adhesion. (B) Myosin-IIA levels also increase with matrix μ-elasticity, unless inhibited by Blebb (i) or by knockdown (ii: siMIIA), which suppress lamin-A,C on soft and stiff gels. (C) MSCs transduced with GFP-lamin-A were knocked down for lamin-A,C and cultured on soft-and-thick (0.3 kPa), soft-and-thin (2–3 μm), or stiff (40 kPa) gels for 36 h, and then fixed and immunostained. High lamin-A,C–expressing cells show diffuse cytoplasmic LBR (green frames; image contrast is readjusted to show cytoplasmic pool); low lamin-A,C–expressing cells show nucleus-localized LBR (red frames). (D) Overexpression and knockdown allow lamin-A,C levels to be controlled independent of matrix. (i) Nuclear projected area increases with the lamin-A,C level on a given matrix but is greatest on stiff matrices at any given lamin-A,C level. Hyperbolic fits of form $a = a_0 + b \cdot x / (K + x)$ intersect at $x = 0$, which then nuclear height varies as $H \sim 1/A^{1.5}$, but this is not consistent with initial measurements that show weak increases in average nuclear height upon rounding (Figure 1A). DNA concentration and nuclear volume are thus unlikely to change much as nuclei round up. The approach needs to be applied more widely in efforts to assess whether nuclear volume and [DNA] remain constant (or not) as nuclear tension differences and other changes occur for soft versus stiff matrices.

**Apparent microelasticity of matrix regulates relaxed versus contractile cell states**

A biophysical picture is emerging in which stiff matrices including soft-and-thin matrices strongly favor a contractile phenotype owing to an increase in the apparent μ-elasticity sensed by a cell (Figure 8A). Expression levels of nonmuscle myosins in cells on stiff matrices increase with assembled filaments that are stabilized by high tension (Raab et al., 2012). Stiff matrices thereby enhance cell-generated traction forces (Engler et al., 2006; Solon et al., 2007) that exert a tension on the nucleus that is evident as the nucleus is thus pulled and flattened against the matrix. Lamin-A,C responds by increasing on stiff or thin matrices, mirroring tissue profiles (Swift et al., 2013), and conferring nuclear rigidity. Additional factors in the cytoplasm and extracellular matrix might also contribute to nuclear mechanical properties and likely to mechanosensing. Such factors range from nesprins that transfer tension to the nucleus (Starr and Fridolfsson, 2010) to at least one matrix metalloprotease, MMP14 (Gutiérrez-Fernández et al., 2015), that when knocked out in mice leads to increases in collagen fibers (in heart), nesprins, and lamin-A,C levels, consistent with a stiff, fibrotic
Interestingly, lamin-A,C knockdown in human MSCs increases MMP14 transcripts (Figure 4B), but the effect is very noisy compared to LBR, suggesting a more direct regulation of the latter.

Coordinated changes in the cytoskeleton and nuclear lamina contribute to matrix-directed cellular differentiation toward soft versus stiff tissue lineages (Engler et al., 2006; Gilbert et al., 2010), and some aspects of mechanism are becoming clearer. As a nuclear mechanosensor, lamin-A,C orchestrates matrix-directed remodeling of both the nuclear envelope and cytoskeletal reorganization. Down-regulation of lamin-A,C results in suppression of myosin-IIA levels, which in turn relaxes cell contractility to feedback on lamin-A,C. Additionally, LBR levels are elevated with translocation of cytoplasmic pools toward the nuclear envelope. Tissue profiles of LBR expression thus reflect a correlation with tissue softness that anti-correlates with lamin-A,C levels.

Fat is indeed soft, and so it is intriguing that LBR has a carboxy-terminal sterol reductase domain for lipid biosynthesis, consistent with increasing LBR expression levels observed during adipogenic differentiation (Subramanian et al., 2012). Like fat, the brain is very soft and also makes its own cholesterol, amounting to 30% of whole-body levels (Bjorkhem and Meaney, 2004). High LBR and low lamin-A,C in the brain (Figure 3C) is consistent with the complementarity of these two nuclear envelope factors that is evident in adipogenesis (Figure 5C). In contrast, stiff tissues express high lamin-A,C, high myosin-IIA, and low LBR that reflect the more contractile phenotype of cells in stiffer tissues such as bone (Figures 1A, 4, 5, and 7).

Knockdown of lamin-A,C in MSCs on rigid plastic not only suggests an induction away from an osteoblastic phenotype toward a more adipogenic favored phenotype, but the transcriptome changes suggest a phenotype that promotes bone degradation by osteoclasts (Supplemental Figure S8A) consistent with the noted up-regulation of osteopontin (SPP1 in Figure 4B).

LBR is downstream from lamin-A,C mechanosensing

Lamin-A,C and LBR were found here in three different analyses of tissues or MSCs on different matrices to fit a competitive binding model in terms of either lamin-A,C protein or transcript (Figures 4–7). Anti-correlations between these two nuclear envelope components have been noted before (Olins et al., 2001; Zwerger et al., 2008) and most recently found to be almost interchangeable in tethering heterochromatin to phenotype.
the nuclear envelope (Solovei et al., 2013); lack of both proteins generally leads to centralized heterochromatin. In early (E8–E17) embryonic lineages where observations could be made in these studies, LBR is detectable, but in tissues that are subject to early mechanical stress LBR decreases as lamin-A,C increases. The observations include stiff tissue cells such as those of adult cartilage and bone, and myotubes, cardiomyocytes, and smooth muscle as well as endothelial cells subject to flow stresses, but not the earliest muscle stem cells (satellite cells), or the earliest intestine or skin cells, which are all softer tissues. However, the reasons for these expression patterns had not yet been explained. The initial systematics is perhaps clear from the results here: when and where mechanical stress is high in a tissue, lamin-A,C is favored, which inhibits LBR at the protein and transcript level.

LBR interactions with lamin-B are well established and although the site of interaction remains unclear (Worman et al., 1988; Georgatos et al., 1989; Ye and Worman 1994), the findings here lead us to hypothesize that LBR competes with lamin-A,C for binding lamin-B. Heterotypic interactions between lamin-A,C and B-type lamins have also long been reported (Fisher et al., 1986; Georgatos et al., 1988) and are facilitated by the unstructured N-termini that precede the coiled-coil, dimerizing rod domains. Phosphorylation of lamin-A,C in both the N- and C-termini drive disassembly in mitosis and in interphase mechanosensing of soft microenvironments (Buxboim et al., 2014), which will thereby enable binding of LBR to B-type lamins.

LBR transcription could occur through the binding of transcription factor SREBP1 (sterol regulatory element-binding protein 1), which chromatin-IP has shown to bind the LBR promoter (Supplemental Figure S8B; Rosenbloom et al., 2013); SREBP1 also associates with lamin-A,C and is visually sequestered in high-density aggregates of lamin-A,C (Lloyd et al., 2002; Yang et al., 2013). SREBP1 might thus be sequestered by lamin-A,C at the nuclear envelope and be released to bind promoters only when stiffness, stress, and therefore lamin-A,C are low, thereby promoting expression of LBR (Figure 8B). Understanding such a mechanosensitive process thus requires continued efforts at quantifying cytoskeleton-generated nuclear tension.

**MATERIALS AND METHODS**

**Isolation of fresh MSCs from bone marrow**

Bone marrow aspirates were obtained from posterior iliac crest of human donors (University of Pennsylvania School of Medicine) under the procedures and regulations defined by the Helsinki agreement. Mononucleated cells (MNCs) were obtained using a Ficoll density gradient (Ficoll-Paque PLUS; GE Healthcare) and depleted from CD34-positive cells by a Micro-bead kit (Direct CD34 Progenitor Cell Isolation Kit; Miltenyi Biotec) and screened by automated cell sorting from the mononucleated fraction of donor bone marrow cells. Fresh human CD34-positive cells were obtained by cell sorting from the mononucleated fraction of donor bone marrow cells. Cells were cultured for 7 d with stem cells factor (SCF) and thrombopoietin (TPO) for 4 d.

**Glass coverslips silanization and polyacrylamide gel preparation**

The preparation of polyacrylamide (PA) gels with controlled elasticity, thickness, and covalent attachment to glass coverslips is described in detail in a published methods paper (Buxboim et al., 2010b). In brief, glass coverslips (thickness #1.5; Fisher Scientific) were placed in boiling ethanol for 10 min, rinsed in distilled water (DW), and immersed in RCA (DW, hydrogen peroxidase [30%; Fisher Scientific], ammonium hydroxide [30%; Fisher Scientific] at 3:1:3 [vol/vol/vol]) at 80°C for 10 min and rinsed in DW. To remove water traces, glasses were rinsed in ethanol and then in chloroform and silanized in 0.1% allyltri chlorosilane (ATCS; Aldrich) in chloroform (Fisher Scientific) for 30 min. Silanized glasses were then rinsed in chloroform → ethanol → DW and dried under vacuum. Successful silanization can be evaluated by assessing hydrophobicity, for example, by water droplet contact angle. PA gel precursors were prepared by mixing acrylamide (AA, 40%; Sigma) and N,N ’-methylenbisacrylamide (bis-AA, 1.5% [wt/vol] in DW; Sigma) in PBS (Sigma). Nominal gel elasticity was specified by varying acrylamide and cross-linker concentrations as calibrated by desktop rheometer: 0.3 kPa, 7.5% AA, 4.7% bis-AA; 1 kPa, 9% AA, 5.6% bis-AA; 3 kPa, 11.2% AA, 7% bis-AA; 10 kPa, 15% AA, 9.3% bis-AA; 40 kPa, 2.5% AA, 20% bis-AA. Gel thickness was specified by varying the volume of gel precursor and by using 1-µm-diameter monodispersed silica microsphere spacers (Thermo Scientific) as calibrated by confocal imaging (Buxboim et al., 2010b). Gelation was initiated by adding 0.1% (vol/vol) tetramethylethylenediamine (TEMED; Sigma) and 0.1% (wt/vol) ammonium persulfate (Sigma) to gel precursor just before placing it at the center of the silanized coverslips and covering with RCA-treated glasses. Thin gels were cured with weights placed on top of the cover glasses, pressing them against the beads spacers. Gels were allowed to polymerize while covalently binding the silanized glasses for 30–60 min. Nonsilanized glasses were gently removed after immersing in PBS for 1–2 h.

**Gels collagen coating and sterilization**

Gels were immersed in 10 mg/ml sulfo-SANPAH (Fisher Scientific) in 50 mM, pH 8.5, HEPES and reacted under 365 nm i-line exposure for 10 min. Collagen was mixed in 0.1 M acetic acid (Fisher Scientific) at equal volume and in 50 mM, pH 8.5, HEPES to reach 0.2 mg/ml final concentration. Gels were immersed with collagen while agitated overnight at 37°C. Prior to seeding cells, gels were UV-sterilized (cell-culture hood UV light source) for 3 h. During all preparation steps, gels were maintained in a hydrated state.

**Nuclear height model of spreading for an invariant cell-to-nuclear volume ratio**

The projected area of the cell is seen to scale linearly with the projected area of the nucleus regardless of matrix elasticity or adhesion time (e.g., Figure 1Aii). Designating the projected area of the nucleus in state n as \( p_n \) and that of the cell as \( P_n \), the proportionality constant is the slope \( s \) between the projected areas of cells and nuclei in any two states:

\[
P_n = (P_2 - P_1) / (p_2 - p_1) = \text{constant in experiments} \quad (1)
\]
In this nuclear height model (Nucl-Ht Model), nuclear height limits the spreading of the cell and its nucleus. We designate cell height as $A_n$ and nuclear height as $a_n$, so that $A_n = a_n$ is consistent with observations. For simplicity, we approximate the nucleus by an ellipsoid of volume $v_n = \frac{4}{3} \pi b_n c_n$ and that of the cell by half of an ellipsoid $V_r = \frac{2}{3} \pi a_r b_r c_r$. Projected areas are $p_n = \pi b_n c_n = \frac{3}{4} v_n/a_n$ and $P_r = \pi b_r c_r = \frac{3}{2} V_r/A_n$. Hence,

$$s_{\text{model}} = \frac{P_l}{P_r} \left( \frac{V_r}{V_l} \right) \left( \frac{a_l/a_2}{2} - 1 \right) \left( \frac{v_l/v_1}{a_l/a_2} - 1 \right)$$

Althought the choice of state 1 is arbitrary, we obtain the most accurate measurements of projected areas in the maximally spread state, so that $(P_l/p_l) = (P_{\text{max}}/P_{\text{nm}})$. Importantly, we observe that $s_{\text{expt}} = (P_{\text{max}}/P_{\text{nm}})$ within 10%, which implies that the ratio of terms in square brackets is near unity, thus reducing Eq. 2 to

$$(V_r / V_l) = (v_l / v_1) (A_{\text{cell}} / A_{\text{nuc}}) = \text{constant}$$

The Nucl-Ht Model thus reveals an invariant ratio of cell-to-nuclear volume. Such a ratio is often considered phenotypic of cells and is characteristically small for cells such as blood stem cells but generally much larger for various mesenchymal cells. Indeed, with chondrocytes embedded in agarose, osmotically driven changes in cell and nuclear volume (Irianto et al., 2013) also indicate proportional changes in volume ($\sim 300$ mOsm ($\sim 300$ mOsm). The Nucl-Ht Model with the deduced invariance of cell-to-nuclear volume implies that factors that control nuclear height, such as nuclear stiffness conferred by laminas or stress applied by the cytoskeleton, will generally regulate spreading of both the cell and its nucleus.

Transcriptional profiling by titrated DNA microarrays
Total RNA was extracted from cells using Trizol and purified by RNeasy (Qiagen) with on-column DNase digestion according to manufacturer's protocol. Adhesive cells were gently scraped in Trizol. Total RNA was amplified and converted to cDNA using WT-Ovation Pico kit (NuGen). Fragmented and biotin-labeled ST-cDNA was generated using WT-Ovation Exon Module (NuGen). Titrated X/3, 2X/3, and 2X hybridization cocktails (42 µl each) were prepared with 20, 40, and 120 ng/µl ST-cDNA, respectively. Eukaryotic hybridization controls (GeneChip) were included at proportional concentrations. Each sample was interrogated by a series of hybridization, rinse, and scan cycles in which X/3, 2X/3, and 2X titrated hybridization cocktails were applied sequential to individual human gene 1.0 ST DNA microarrays (Affymetrix). Two additional rinse-scan cycles were included in which only hybridization buffer was applied to the arrays (42 µl). Hybridization, washing, and array scanning were performed according to the manufacturer's instructions. Transcriptional profiling of mouse and human tissues was obtained from Affymetrix (publically available data). Original and public gene expression data sets were RMA-summarized.

Immunostaining
Cells were fixed with 3.7% formaldehyde (Sigma-Aldrich) in PBS for 10 min at room temperature (RT) followed by PBS washing 2x for 5 min. Blocking and primary antibody staining were performed in 1% bovine serum albumin in PBS. Primary antibody concentrations ranged between 1/300 and 1/500, depending on the stock concentration, and all primary antibodies were incubated at RT for 2 h or overnight at 4°C. All donkey secondary antibodies (Alexa Fluor dyes 488, 564, and 647) were stained for 1–2 h at RT at 1:500 dilution in PBS and TRITC-phalloidin (Sigma-Aldrich) was used at a concentration of 100 ng/ml. Imaging for quantitative immunofluorescence of lamin-A,C, myosin-IIA, and LBR was performed using an inverted microscope (IX-71; Olympus) with either 20X (Olympus; NA 0.75) or 40X (NA 0.60) objectives, and a cooled charge-coupled device (CCD) camera (Cascade; Photometrics) and image acquisition was performed with Image Pro software (Media Cybernetics). Fixed cells were immunostained using the following antibodies and reagents: myosin-IIA (mouse), monoclonal HSP90A1, polyclonal SYNE1 (Abcam); polyclonal myosin-IIA, monoclonal lamin-A,C (mouse), polyclonal lamin-A,C (goat), polyclonal lamin-B1, polyclonal cleaved lamin-A,C (Santa Cruz); polyclonal LBR (Novus Biologicals); phalloidin (Sigma). Fixed cells were mounted in mounting medium (Axell). To prevent volume distortions, samples prepared for confocal z-stacks quantification were not mounted.

Quantitative immunofluorescence
Lamp intensity and field of view homogeneity were calibrated relative to a fluorescent plastic standard pixel by pixel per each experiment. Image analysis was performed by a Matlab-based (Mathworks) custom designated application that included background subtraction, cell and nucleus objects registration and intensity integration, morphological and statistical analyses.

Immunoblotting
Cells were trypsinized, pelleted, and stored at −20°C until analysis. Pellets were thawed and resuspended in 1X LDS lysis buffer supplemented with 1% protease and 1% phosphatase inhibitors and sonicated on ice (3 × 15 s pulses, intermediate power setting). After resting for 30 min on ice, samples were denatured at 80°C with 0.5% β-mercaptoethanol (vol/vol) for 10 min. Samples were loaded onto bis-Tris 4−12% gradient gels for electrophoresis (100 V × 10 min; 160 V × 55 min) and then blotted (iBlot; Life Technologies; settings P3, 7 min) onto blotting membrane. Band intensities were quantified using Fiji/ImageJ, relative to local background levels flanking the specific bands.

Mass spectrometry
SDS-PAGE gels (NuPAGE 4−12% bis-Tris; Invitrogen) were run at 100 V for 10 min and 160 V for 25 min. Gel sections were washed (50% 0.2 M ammonium bicarbonate [AB] solution, 50% acetonitrile [ACN], 50 min at 37°C), dried by lyophilization, incubated with a reducing agent (20 mM tris(2-carboxyethyl)phosphine [TCEP] in 25 mM AB solution at pH 8.0, 15 min at 37°C), and alkylated (40 mM iodoacetamide [IAM]) in 25 mM AB solution at pH 8.0, 30 min at 37°C). The gel sections were dried by lyophilization before in-gel trypsinization (20 µg/ml sequencing grade modified trypsin in buffer as described in the manufacturer’s protocol [Promega], 18 h at 37°C with gentle shaking). The resulting solutions of tryptic peptides were acidified by addition of 50% digest dilution buffer (60 mM AM solution with 3% methanolic acid).

Peptide separations (5 µl injection volume) were performed on 15-cm PicoFrit column (75 µm inner diameter; New Objective) packed with Magic 5 µm C18 reversed-phase resin (Michrom Bioreources) using a nanoflow high-pressure liquid chromatography system (Eksigent Technologies), which was coupled online to a hybrid LTQ-Orbitrap XL mass spectrometer (Thermo Fisher Scientific) via a nanoelectrospray ion source. Chromatography was performed with solvent A (Milli-Q water with 0.1% formic acid) and solvent B (acetonitrile with 0.1% formic acid). Peptides were eluted at 200 nL/min for 3−28% B over 42 min, 28−50% B over 26 min, 50−80% B over 5 min, 80% B for 4.5 min before returning to 3% B over 0.5 min. To minimize
sample carryover, a fast blank gradient was run between each sample. The LTQ-Orbitrap XL was operated in the data-dependent mode to automatically switch between full scan MS (m/z = 350–2000) in the Orbitrap analyzer (with resolution of 60,000 at m/z 400) and the fragmentation of the six most intense ions by collision-induced dissociation in the ion trap mass analyzer.

Raw mass spectroscopy data was processed using Elucidator (version 3.3; Rosetta Biosoftware). The software was set up to align peaks in data from samples derived from corresponding molecular weight regions of the 1D gels. Peptide and protein annotations were made using SEQUEST (version 28; Thermo Fisher Scientific) with full tryptic digestion and up to two missed cleavage sites. Peptide masses were selected between 800 and 4500 amu with peptide mass tolerance of 1.1 amu and fragment ion mass tolerance of 1.0 amu. Peptides were searched against a database compiled from UniRef100 (November 2010) mouse, plus contaminants and a reverse decoy database. A delta Cn of 0.01 and mass error limit of 20 ppm was used, resulting in a false-positive rate of ~10%. In these experiments, only proteins detected with three or more peptides were considered. The peptide database was modified to search for alkylated cysteine residues (monoisotopic mass change; Δ = +57.021 Da) and oxidized methionine (Δ = +15.995 Da). In proteomic profiling experiments, we also considered the acetylation oflysine (Δ = +42.011 Da), methylation oflysine and arginine (Δ = +14.016 Da), and phosphorylation ofserine, tyrosine, threonine, histidine, and aspartate (Δ = +79.966 Da). Ion currents of modified peptides were summed with their parent peptide. Peptides derived from trypsin or keratin were considered to be contaminants and were not used in subsequent calculations. When evaluating total ion current, only signals from annotated peptides were summed. The PRF algorithm was coded for Mathematica (version 8; Wolfram Research) and was used for all MS protein quantitation (Shin et al., 2011).

siRNA and short hairpin RNA knockdown of MYH9, LMNA, LBR, and inhibitors

All siRNAs used in this study were purchased from Dharmacon. Cells were passaged > 24 h before transfection and incubated with a complex of siRNA (30 nM; siLMNA: 5'-GGUGUGUGAGCAUCGUGGCU-3'; siMYH9: 5'-GGCCAAACCCUGCGAAUAAUU-3' with complement sequence 5'-UUUUUGCGAGGUGGCUU-3'; scrambled-siRNA siGENOME nontargeting siRNA #1 [Thermo Fisher Scientific]) or shLBR (TRCN0000060460; Sigma) and 1 μg/ml Lipofectamine 2000 according to the manufacturer's instructions for 24 h (in low-glucose DMEM with 10% FBS). Racemic blebbistatin (EMD) was used at 30 μM. For shLMNA treatment, A549 cells were infected with lentiviral supernatants targeting lamin-A:C (TRCN0000061833; Sigma) at a multiplicity of infection (MOI) of 10 in the presence of 80 μg/ml polybrene (Sigma), and cultured for 24 h. The cells were then selected by 2 μg/ml puromycin (Sigma) for 30 d.

Transfection and transductions of lamin-A

A construct expressing GFP-lamin-A under the EF1α promoter (Izumi et al., 2000) was packed into a lentiviral delivery system. Cells were transduced at MOI 50 and evaluated for survival and proliferation. The fraction of GFP-lamin-A–positive cells before experiment was ~50%. Colonies of GFP-lamin-A–expressing MSCs were isolated using a cloning cylinder (Bel-Art Products, Pequannock, NJ), trypsinized and further expanded for experiments. Lamin-A constructs were transfected via electroporation following manufacturer's protocols (MSCs kit, Nucleofector; Lonza). Lamin-A transfections of A549 cells and all myosin-IIA constructs in MSCs transfections used Lipofectamine LTX (Invitrogen) with Plus reagent using 0.5 g DNA per well in a six-well plate. Transfection levels were similar across all constructs (within 20–30%) based on GFP densitometry of Western blots.

Transwell migration

For migration through transwells (Corning), A549 cells were seeded at 300,000 cells/cm² onto the top side of the filter membrane and left to migrate in normal culture condition for 24 h.

Confocal microscopy and deconvolution of fixed samples

Laser scanning confocal fluorescence microscopy was carried out using the following systems: Leica Microsystems TCS SP8, 63× / NA 1.4 oil immersion objective (Figures 1Ai, iii and 2Ei). Nuclear orthogonal view was generated from 0.21 μm z-stack and constructed using Fiji (Schindelin et al., 2012). To evaluate the corresponding nuclear roughness spectra, iterative self-organizing data algorithm thresholding (Ridler and Calvard, 1978) was applied and nuclei were horizontally aligned per fitted ellipses. Apical and dorsal nuclear perimeter contours were obtained while discarding 25% edge regions, and roughness Fourier spectra were evaluated and smoothed using Matlab. Epi-fluorescence deconvolution was applied using the Deltavision Deconvolution IX70 Olympus system (Figure 1A).

Rheology

The nominal elasticity of the gels was calibrated using a strain-controlled rheometer (TA instruments; RFS-II). A flat titanium plate, 25 mm diameter, was used with 0.5 ml sample volume and 0.95 mm gap. Platform surface temperature was set to 25°C, with 0.1% strain and 1 rad/s rate.

Apparent μ-elasticity of thin gels

A detailed description of the AFM force-indentation measurements was published in a methods paper (Buxboim et al., 2010b). In brief, AFM (MFP-3D; Asylum Research) force-indentation curves were obtained using pyramidal tip cantilevers (kp ~ 24 pN/nm, TR400PB; Olympus). Force-indentation data was exported to Matlab for computing the apparent μ-elasticity. The Young’s modulus E was calculated by fitting (MatLab) the classical parabolic Hertz model (Hertz, 1882) assuming a Poisson ratio of ν = 0.5 as we estimated for PA gels (Buxboim et al., 2010b) and a pyramidal indenter (Domke and Radmacher 1998; Rehfeldt et al., 2007):

$$E = \frac{\pi (1-\nu^2) F}{2\delta^2 \tan(\alpha)}$$

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REFERENCES

Supplementary figure legends

Figure S1: Myosin-IIA is essential for cell & nucleus mechanosensitivity of matrix stiffness

(A) Representative images of MSCs spreading more on stiff gels and less on soft gels after 36 hours in culture but not if treated with Blebb myosin-II inhibitor. Scale-bar: 40 μm. (B) Projected areas of (i) cells and (ii) nuclei increase monotonically with matrix stiffness but Blebb-treated cells show no matrix-dependence. Both cellular and nuclear spreading areas of MSCs satisfy hyperbolic fits with half spreading response elasticity $E_0 = 3.3$ kPa. (C) Immunofluorescence images of MSCs expanded on plastic for 2-8 weeks are shown here at passage P2, P4 and P7 after 36 hours of culture on gels. Scale-bar: 20 μm. (D) While maintaining a linear correlation between nucleus and cell projected areas, the canonical spreading hierarchy soft $<$ thin $<$ stiff is satisfied predominantly at early passage whereas P7 cells altogether exhibit larger spreading areas than early passage cells. Inset: the ratio between cells projected areas that are obtained for soft versus stiff gels reflects the extent of cellular mechanosensitivity to matrix stiffness. Soft-to-stiff spreading ratio of late passage cells is close to 1, yet P2 cells spread three-fold more on stiff gels compared to soft. (E) Cellular mechano-sensitivity and senescence: MSCs were expanded in culture for 8 weeks (standard plastic flasks) during which cells underwent 7 passages (P7). To interrogate cellular mechanosensitivity, MSCs were trypsin-detached at passage P2, P4 and P7, cultured for 36 hours on soft (1 kPa), soft and thin (2-3 μm, apparent μ-elasticity 6 kPa) and stiff (40 kPa) gels and lamin-A,C levels were evaluated by quantitative immunofluorescence (qIF). Low passage P2 MSCs show maximal mechanosensitivity, as exemplified relative to the passage-mean trend (black), which diminishes with increasing passage.

Figure S2: Cell spreading & nucleus flattening dynamics during matrix engagement and adhesion

(A) Following seeding, the dynamics of cell spreading and nucleus stretching during adhesion to glass surfaces satisfies a hyperbolic fit, with $t_{1/2} = 45$ min half time both for cell and nucleus projected areas. (A-ii) The cell-to-nucleus projected area ratio dynamics also obeys a $t_{1/2} = 45$ min hyperbolic fit. As cells spread, cell-to-nucleus projected area increases from 3.3 to 16. Non-adherent cells correspond to $t \to 0$ limit. Under the assumption that cells and nuclei are rounded in suspension, we conclude that nucleus volume is 6 fold smaller than cell volume.

Figure S3: Fresh MSCs are isolated from human bone marrow donors and cultured within hours

Bone marrow cells are isolated from fresh aspirates and purified by rinse. Mono-nucleated CD34-depleted cells (see methods) were allowed to settle down for 30 min and engage collagen-coated soft-thin gels (1 kPa, 2-3 μm) followed by 3-4 hours of agitation. To screen for strongly adhesive cells, gel substrates were immersed in PBS and positioned perpendicular to the plane of agitation. Gels were subjected to flow-induced stress for 0-to-20 min. Cells were then re-immersed in medium, incubated for 12 hours and fixed and immunostained. (A) Representative images show a transition from a rounded to a prototypical mesenchymal dendritic morphology with increasing flow time. Scale-bar: 40 μm. (B) (i) Flow-induced stress is shown to remove ~50% of the cells but the prolongation of flow shows no accumulative effect, consistent with the removal of weakly adherent cells already after < 2.5 minutes. The fraction of attached cells is computed relative to the number to seeded cells. (ii-iii) In response to the mechanical stresses that are induced by flow, cell projected area and lamin-A,C levels increase concomitantly with nucleus projected area (cell/nucleus...
projected area slope 30) with rinse time. This increase in spreading and in lamin-A,C levels is reminiscent of the transition between ‘soft’ to ‘stiff’ cellular phenotypes which is shown above to be induced by matrix stiffness or thinness, and consistent with matrix adhesion and spreading dynamics and molecular and drug perturbations of lamin-A and myosin-II (sketched in Fig. 4A-i). (C) Plastic-adhering colony-forming isolated cells were expanded in standard plastic flasks and interrogated by flow cytometry. Cells express MSC surface markers (CD105, CD166, CD44, CD90) and lack expression of hematopoietic markers (CD34, CD45RA) as calibrated versus secondary antibody controls.

Figure S4: Validation of lamin-A,C overexpression and knockdown, myosin relaxation and nucleus stiffening

(A, i) Bimodal distribution confirms lamin-A-GFP transfection of 30% of the cells. (ii) A decrease in GFP intensity and a left shift of the GFP-positive cells distribution is induced by siLMNA knockdown. (B) Immunoblot confirms lamin-A transduction, showing a GFP-conjugated lamin-A band. (C) DNA microarray transcript profiling of blebbistatin-treated versus non-treated MSCs: cell relaxation decreases myosin-IIA and LMNA RNA levels but not LBR. (D) The more GFP-lamin-A is expressed, the stiffer the nucleus becomes as evaluated by micropipette aspiration measurements. The extent of nuclear deformation in A549 lung epithelial cells was evaluated after 180 sec of aspirating nuclei that express GFP-lamin-A over a range of > 10 fold. Fits of the stiffening of the nucleus as a function of the increase in lamin-A levels above the average wild-type level indicates a 0.5 power law.

Figure S5: Lamin-A,C and Myosin-IIA maintain cytoskeletal-nucleoskeletal feedback

(A) After just 2 hrs of adhesion and spreading, lamin-A,C and myosin-IIA levels increase in MSCs. Myosin-II inhibition subsequently suppresses both proteins. (B) With cell adhesion and spreading lamin-A,C and myosin-IIA levels both increase by 1-2 hrs unless lamin-A,C is knocked down (KD). Plots show single-cell quantitative immunofluorescence intensities (n ~ 50 cells per condition), with myosin-IIA suppression at 36 hrs confirmed by immunoblot (above) and by Mass Spectrometry (below) averaged over of multiple tryptic peptides (detected in 60-80 kDa range).

Figure S6: Modulation of Lamin-A and LBR leads to change of LBR per LMNA stoichiometry

(A) LBR (red) were depleted in A549 cells by the shLBR treatment. (B) Knockdown of Lamin-A by shLMNA leads to an increase in LBR per LMNA stoichiometry, while knockdown of LBR decreases the stoichiometry (n > 200 cells per group).

Figure S7: Analyses of nuclear shape and volume of MSC’s after lamin-A,C knockdown, based on fluorescence intensity of Hoechst-labeled DNA and an assumption of ellipsoidal shapes.
Figure S8: Less bone and more fat with low lamin-A,C: MSCs and osteoblasts favor bone resorption by osteoclasts after LMNA knockdown, and the transcription factor sterol response binding protein-1 (SREBP1) promotes expression of LBR in the lipid biosynthesis pathway.

(A) MSCs and osteoblasts contribute to bone resorption via osteoclasts (Roux and Orcel 2000, Teti 2013), and lamin-A,C knockdown in MSCs on rigid plastic favors such a process relative to control cells. Osteoclast precursors differentiate in the presence of macrophage colony-stimulating factor, M-CSF: deficient mice develop an osteopenosis that is characterized by the absence of osteoclasts, and local injections of M-CSF in bone increase in situ osteoclast differentiation and bone resorption. Osteoprotegerin (TNFRSF11B) reduces the production of osteoclasts by inhibiting the differentiation of precursors. CTHRC1 expression in bone is blunted by aging where bone resorption tends to dominate, and it is stimulated by treatment with soluble RANKL (TNFSF11) with an initial phase of bone resorption. Hepatocyte growth factor (HGF) signals human osteoblasts to express osteopontin (SPP1), with inhibition of the HGF receptor (MET) decreasing osteopontin production. A role for the transcription factor vitamin-D receptor (VDR), such as in expression of RANKL, is likely given that 1,25-dihydroxyvitamin-D3 together with parathyroid hormone increase bone resorption, primarily via an indirect mechanism mediated by osteoblasts. Many other genes are involved but most or all do not change as much as the indicated genes after lamin-A,C knockdown in the MSCs.

(B) Screenshot of ENCODE data showing ChIP-Seq results for SREBP1 binding to the promoter region of LBR gene.

Supplementary References
Figure S1

Cell & nuclear morphology of MSCs respond to matrix elasticity unless myosin-II is inhibited.

A

B

(i) Cell
(ii) Nucleus

Projects area [µm²]

Blebb.

C

D

E

Early-passage MSCs are highly mechanosensitive

Passage-mean trend

Lamin-A,C [a.u.]

Nucleus projected area [µm²]

Cell projected area [µm²]

Aparent µ-elasticity [kPa]

Passage-mean trend

Myosin-IIA

Actin

Lamin-A,C

Soft/Stiff cell area

slope = 27.4
Cells spread and nuclei flatten within < 1 hr of adhesion

Figure S2

A

(i) Cells spread and nuclei flatten within < 1 hr of adhesion

(ii) Cell / nucleus projected area ratio

- Cell $t_{1/2} = 45$ min
- Nucleus $t_{1/2} = 45$ min

$V_{cell} / V_{nuc} = 6$
Figure S3

--- Fresh MSCs are adherent and mechanosensitive ---

(A) Shear rinse:

0 min 2.5 min 10 min 20 min

Actin Vimentin Lamin-A,C

--- Surface markers confirm MSCs ---

(B) (i) Fraction of attached cells

Fraction of attached cells

Rinse time [min]

(ii) Cell projected area [µm²]

0 to 5 min 10 to 20 min

0 10 20

1500 2500

(iii) Lamin-A [a.u.]

0 to 5 min 10 to 20 min

1 0.8 0.6

Rinse time [min]

Fraction of attached cells

(C) Donor-1 Donor-2 Donor-3

Surface markers confirm MSCs
Figure S4

Validation of Lamin-A,C KD and OE and blebb treatment

A

(i) Transduced

(ii) Transduced & siLMA

B

WT Transduced

GFP-Lamin-A
HSP90AB1
Lamin-A,C

C

MYH9LMNALBR
HSP90AB1GAPDH

D

10^0

10^1

10^2

10^3

10^4

Lamin-A-GFP [a.u.]

ΔElasticity [kPa]
Lamin-A,C and myosin-IIA maintain a feedback relationship

Figure S5

A

B

Immunoblotting (36 hr):
- siLMNA WT
- Lamin-A,C
- Myosin-IIA
- β-Actin

Mass Spectrometry (36 hr):
- KD/SC
- #peptides
  - Lamin-A,C: 23±3% 44
  - Myosin-IIA: 56±12% 16
Figure S6

Modulation of LBR per LMNA stoichiometry

A

DNA | LBR | Lamin-A,C

WT

shLBR

B

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<thead>
<tr>
<th></th>
<th>WT</th>
<th>shLMNA</th>
<th>shLBR</th>
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<td>LBR per LMNA</td>
<td>1.0 ± 0.1</td>
<td>2.0 ± 0.1</td>
<td>0.9 ± 0.1</td>
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Modulation of LBR per LMNA stoichiometry
**Figure S7**

**Shape and Intensity analyses:** Nuclear Height * [DNA conc] ~ 1 / Area

This population used for following plots. DNA amount ~ constant but [DNA conc] = DNA / V could vary with variation of Nuclear Volume V

Fluorescence Intensity: $I_{\text{tot}} = \phi V \text{[DNA conc]}$

$I_{\text{tot}} / A = \frac{2}{3} \phi H \text{[DNA conc]}$

expt: $I_{\text{tot}} / A = \frac{\text{const}}{A} = \text{const} \phi H \text{[DNA conc]}$

Ellipsoid Approximation:

Volume $V = \frac{4}{3} \pi a b c$

Projected Area $A = \pi a b$

Height $H = 2 c = \frac{3}{2} V / A$

Fluorescence Intensity: $I_{\text{center}} = \phi \alpha H \text{[DNA conc]}$

expt: $I_{\text{center}} / I_{\text{tot}} = 18 \mu m^2 / A$

Intensity Test of Ellipsoid Approximation:

Fluorescence $H / V = 18 \mu m^2 / \alpha A$

Ellipsoid $\left(\frac{3}{2} / A\right) (12 \mu m^2 / \alpha)$

$y = 18 / x$

$R^2 = 0.9$

$R^2 = 0.8$
Figure S8

Bone loss is favored by Lamin-A,C knockdown

A

**Osteoclast** precursor from Soft hematopoietic Marrow

- **RANK**
- **RANK Ligand**
- **TNFRSF11B** Osteoprotogerin (OPG)

**Osteoclast**: multi-nucleated, giant cell in frustrated phagocytosis on Rigid Bone

**MSC** or **Osteoblast**

Osteoid → Stiff Matrix
calcified collagen matrix = Rigid Bone

- **CSF1** Macrophage Colony Stimulating Factor (M-CSF)
- **CTHRC1**
- **HGF**
- **MET**
- **SPP1** Osteopontin

Knockdown of **LMNA** in MSCs on Rigid Plastic

Log2 (Fold change)

Gene intensity

B

**Adipogenic transcription factor SREBP1 regulates expression of sterol reductase LBR**

**UCSC genome browser ENCODE database.** Screenshot Sept.1, 2017

Transcription Factor ChIP-seq (161 factors) from ENCODE with Factorbook Motifs

Factorbook Link: SREBP1
Factor: SREBP1
Cluster Score (out of 1000): 678
Position: chr1:226615747-226616116
Band: 1q42.12
Genomic Size: 370

View DNA for this feature (hg19/Human)

Assays for SREBP1 in Cluster

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<th>abr</th>
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<th>antibody</th>
<th>treatment</th>
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<td>SREBP1</td>
<td>SREBP1</td>
<td>insulin</td>
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